

SEQUENCE LISTING



<110> Guss, Bengt
Nilsson, Martin
Frykberg, Lars
Flock, Jan-Ingmar
Lindberg, Martin

<120> Fibrinogen Binding Protein Originating from
Coagulase-Negative Staphylococcus

<130> guss 09/147405

<140> 09/147405

<141> 1999-04-01

<150> PCT/SE97/10191

<151> 1997-06-18

<150> SE 9602496-3

<151> 1996-06-20

<160> 15

<170> PatentIn Ver. 2.0

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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22

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<213> Staphylococcus epidermidis

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Val Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile	
20 25 30	
att aaa aaa gaa gaa acg aat aac tac gat ggc ata gaa aaa cgc tca	143
Ile Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser	
35 40 45	
gaa gat aga aca gag tca aca aca aat gta gat gaa aac gaa gca aca	191
Glu Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr	
50 55 60	
ttt tta caa aag acc cct caa gat aat act cat ctt aca gaa gaa gag	239
Phe Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu	
65 70 75	
gta aaa gaa tcc tca tca gtc gaa tcc tca aat tca tca att gat act	287
Val Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr	
80 85 90 95	
gcc caa caa cca tct cac aca aca ata aat aga gaa gaa tct gtt caa	335
Ala Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln	
100 105 110	
aca agt gat aat gta gaa gat tca cac gta tca gat ttt gct aac tct	383
Thr Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser	
115 120 125	
aaa ata aaa gag agt aac act gaa tct ggt aaa gaa gag aat act ata	431
Lys Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile	
130 135 140	
gag caa cct aat aaa gta aaa gaa gat tca aca aca agt cag ccg tct	479
Glu Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser	
145 150 155	
ggc tat aca aat ata gat gaa aaa att tca aat caa gat gag tta tta	527
Gly Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu	
160 165 170 175	
aat tta cca ata aat gaa tat gaa aat aag gct aga cca tta tct aca	575
Asn Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr	
180 185 190	
aca tct gcc caa cca tcg att aaa cgt gta acc gta aat caa tta gcg	623
Thr Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala	
195 200 205	

gcg gaa caa ggt tgc aat gtt aac cat tta att aaa gtt act gat caa	671
Ala Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr Asp Gln	
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agt att act gaa gga tat gat gat agt gaa ggt gtt att aaa gca cat	719
Ser Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His	
225 230 235	
gat gct gaa aac tta atc tat gat gta act ttt gaa gta gat gat aag	767
Asp Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys	
240 245 250 255	
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Val Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn Thr Val	
260 265 270	
cca tca gat tta acc gat agc ttt aca ata cca aaa ata aaa gat aat	863
Pro Ser Asp Leu Thr Asp Ser Phe Thr Ile Pro Lys Ile Lys Asp Asn	
275 280 285	
tct gga gaa atc atc gct aca ggt act tat gat aac aaa aat aaa caa	911
Ser Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln	
290 295 300	
atc acc tat act ttt aca gat tat gta gat aag tat gaa aat att aaa	959
Ile Thr Tyr Thr Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asn Ile Lys	
305 310 315	
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Ala His Leu Lys Leu Thr Ser Tyr Ile Asp Lys Ser Lys Val Pro Asn	
320 325 330 335	
aat aat acc aag tta gat gta gaa tat aaa acg gcc ctt tca tca gta	1055
Asn Asn Thr Lys Leu Asp Val Glu Tyr Lys Thr Ala Leu Ser Ser Val	
340 345 350	
aat aaa aca att acg gtt gaa tat caa aga cct aac gaa aat cgg act	1103
Asn Lys Thr Ile Thr Val Glu Tyr Gln Arg Pro Asn Glu Asn Arg Thr	
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gct aac ctt caa agt atg ttt aca aat ata gat acg aaa aat cat aca	1151
Ala Asn Leu Gln Ser Met Phe Thr Asn Ile Asp Thr Lys Asn His Thr	
370 375 380	
gtt gag caa acg att tat att aac cct ctt cgt tat tca gcc aag gaa	1199
Val Glu Gln Thr Ile Tyr Ile Asn Pro Leu Arg Tyr Ser Ala Lys Glu	
385 390 395	

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Thr Asn Val Asn Ile Ser Gly Asn Gly Asp Glu Gly Ser Thr Ile Ile	
400 405 410 415	
gac gat agc aca ata att aaa gtt tat aag gtt gga gat aat caa aat	1295
Asp Asp Ser Thr Ile Ile Lys Val Tyr Lys Val Gly Asp Asn Gln Asn	
420 425 430	
tta cca gat agt aac aga att tat gat tac agt gaa tat gaa gat gtc	1343
Leu Pro Asp Ser Asn Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu Asp Val	
435 440 445	
aca aat gat gat tat gcc caa tta gga aat aat aat gat gtg aat att	1391
Thr Asn Asp Asp Tyr Ala Gln Leu Gly Asn Asn Asn Asp Val Asn Ile	
450 455 460	
aat ttt ggt aat ata gat tca cca tat att att aaa gtt att agt aaa	1439
Asn Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile Ser Lys	
465 470 475	
tat gac cct aat aag gat gat tac acg act ata cag caa act gtg aca	1487
Tyr Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr Val Thr	
480 485 490 495	
atg cag acg act ata aat gag tat act ggt gag ttt aga aca gca tcc	1535
Met Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser	
500 505 510	
tat gat aat aca att gct ttc tct aca agt tca ggt caa gga caa ggt	1583
Tyr Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly	
515 520 525	
gac ttg cct cct gaa aaa act tat aaa atc gga gat tac gta tgg gaa	1631
Asp Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu	
530 535 540	
gat gta gat aaa gat ggt att caa aat aca aat gat aat gaa aaa ccg	1679
Asp Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro	
545 550 555	
ctt agt aat gta ttg gta act ttg acg tat cct gat gga act tca aaa	1727
Leu Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys	
560 565 570 575	
tca gtc aga aca gat gaa gat ggg aaa tat caa ttt gat ggg gtg cag	1775
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Val Asp

1781

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<211> 593
<212> PRT
<213> Staphylococcus epidermidis

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35 40 45
Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr Phe
50 55 60
Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu Val
65 70 75 80
Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr Ala
85 90 95
Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln Thr
100 105 110
Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser Lys
115 120 125
Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile Glu
130 135 140
Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser Gly
145 150 155 160
Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn
165 170 175
Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr Thr
180 185 190
Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala Ala

195		200		205
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Ala Glu Asn Leu Ile Tyr	Asp Val Thr Phe Glu	Val Asp Asp Lys Val		
245	250	255		
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260	265	270		
Ser Asp Leu Thr Asp Ser	Phe Thr Ile Pro Lys	Ile Lys Asp Asn Ser		
275	280	285		
Gly Glu Ile Ile Ala Thr	Gly Thr Tyr Asp Asn	Lys Asn Lys Gln Ile		
290	295	300		
Thr Tyr Thr Phe Thr Asp	Tyr Val Asp Lys Tyr	Glu Asn Ile Lys Ala		
305	310	315	320	
His Leu Lys Leu Thr Ser	Tyr Ile Asp Lys Ser	Lys Val Pro Asn Asn		
325	330	335		
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340	345	350		
Lys Thr Ile Thr Val Glu	Tyr Gln Arg Pro Asn	Glu Asn Arg Thr Ala		
355	360	365		
Asn Leu Gln Ser Met Phe	Thr Asn Ile Asp Thr	Lys Asn His Thr Val		
370	375	380		
Glu Gln Thr Ile Tyr Ile	Asn Pro Leu Arg Tyr	Ser Ala Lys Glu Thr		
385	390	395	400	
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405	410	415		
Asp Ser Thr Ile Ile Lys	Val Tyr Lys Val Gly	Asp Asn Gln Asn Leu		
420	425	430		
Pro Asp Ser Asn Arg Ile	Tyr Asp Tyr Ser Glu	Tyr Glu Asp Val Thr		
435	440	445		
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Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile Ser Lys Tyr				
465		470		475
				480
Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr Val Thr Met				
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Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser Tyr				
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Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly Asp				
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Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu Asp				
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Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro Leu				
	545		550	555
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Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys Ser				
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<212> DNA

<213> Staphylococcus epidermidis

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gaagatagaa cagagtcaac aacaaatgta gatgaaaacg aagcaacatt ttacaaaag 180

accctcaag ataatactca tcttacagaa gaagaggtaa aagaatcctc atcagtcgaa 240

tcctcaaatt catcaattga tactgcccac caaccatctc acacaacaat aaatagagaa 300

gaatctgttc aaacaagtga taatgtagaa gattcacacg tatcagatct tgctaactct 360

aaaataaaag agagtaacac tgaatctggt aaagaagaga atactataga gcaacctaat 420
 aaagtaaaag aagattcaac aacaagtcag ccgctctggct atacaaatat agatgaaaaa 480
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<211> 581

<212> PRT

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Tyr Asp Gly Ile Glu Lys Arg Ser Glu Asp Arg Thr Glu Ser Thr Thr
35 40 45

Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr Pro Gln Asp
50 55 60

Asn Thr His Leu Thr Glu Glu Glu Val Lys Glu Ser Ser Ser Val Glu
65 70 75 80

Ser Ser Asn Ser Ser Ile Asp Thr Ala Gln Gln Pro Ser His Thr Thr
85 90 95

Ile Asn Arg Glu Glu Ser Val Gln Thr Ser Asp Asn Val Glu Asp Ser
100 105 110

His Val Ser Asp Phe Ala Asn Ser Lys Ile Lys Glu Ser Asn Thr Glu
115 120 125

Ser Gly Lys Glu Glu Asn Thr Ile Glu Gln Pro Asn Lys Val Lys Glu
130 135 140

Asp Ser Thr Thr Ser Gln Pro Ser Gly Tyr Thr Asn Ile Asp Glu Lys
145 150 155 160

Ile Ser Asn Gln Asp Glu Leu Leu Asn Leu Pro Ile Asn Glu Tyr Glu
165 170 175

Asn Lys Ala Arg Pro Leu Ser Thr Thr Ser Ala Gln Pro Ser Ile Lys
180 185 190

Arg Val Thr Val Asn Gln Leu Ala Ala Glu Gln Gly Ser Asn Val Asn
195 200 205

His Leu Ile Lys Val Thr Asp Gln Ser Ile Thr Glu Gly Tyr Asp Asp
210 215 220

Ser Glu Gly Val Ile Lys Ala His Asp Ala Glu Asn Leu Ile Tyr Asp
 225 230 235 240

Val Thr Phe Glu Val Asp Asp Lys Val Lys Ser Gly Asp Thr Met Thr
 245 250 255

Val Asp Ile Asp Lys Asn Thr Val Pro Ser Asp Leu Thr Asp Ser Phe
 260 265 270

Thr Ile Pro Lys Ile Lys Asp Asn Ser Gly Glu Ile Ile Ala Thr Gly
 275 280 285

Thr Tyr Asp Asn Lys Asn Lys Gln Ile Thr Tyr Thr Phe Thr Asp Tyr
 290 295 300

Val Asp Lys Tyr Glu Asn Ile Lys Ala His Leu Lys Leu Thr Ser Tyr
 305 310 315 320

Ile Asp Lys Ser Lys Val Pro Asn Asn Asn Thr Lys Leu Asp Val Glu
 325 330 335

Tyr Lys Thr Ala Leu Ser Ser Val Asn Lys Thr Ile Thr Val Glu Tyr
 340 345 350

Gln Arg Pro Asn Glu Asn Arg Thr Ala Asn Leu Gln Ser Met Phe Thr
 355 360 365

Asn Ile Asp Thr Lys Asn His Thr Val Glu Gln Thr Ile Tyr Ile Asn
 370 375 380

Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile Ser Gly Asn
 385 390 395 400

Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile Ile Lys Val
 405 410 415

Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn Arg Ile Tyr
 420 425 430

Asp Tyr Ser Glu Tyr Glu Asp Val Thr Asn Asp Asp Tyr Ala Gln Leu
 435 440 445

Gly Asn Asn Asn Asp Val Asn Ile Asn Phe Gly Asn Ile Asp Ser Pro
 450 455 460

Tyr Ile Ile Lys Val Ile Ser Lys Tyr Asp Pro Asn Lys Asp Asp Tyr
 465 470 475 480

Thr Thr Ile Gln Gln Thr Val Thr Met Gln Thr Thr Ile Asn Glu Tyr
 485 490 495
 Thr Gly Glu Phe Arg Thr Ala Ser Tyr Asp Asn Thr Ile Ala Phe Ser
 500 505 510
 Thr Ser Ser Gly Gln Gly Gln Gly Asp Leu Pro Pro Glu Lys Thr Tyr
 515 520 525
 Lys Ile Gly Asp Tyr Val Trp Glu Asp Val Asp Lys Asp Gly Ile Gln
 530 535 540
 Asn Thr Asn Asp Asn Glu Lys Pro Leu Ser Asn Val Leu Val Thr Leu
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 <222> (33)..(3308)

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 Leu Leu Thr Lys Lys Lys Pro Ile Ala Asn Lys Ser Asn Lys Tyr Ala
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 Ile Arg Lys Phe Thr Val Gly Thr Ala Ser Ile Val Ile Gly Ala Thr
 25 30 35
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 Leu Leu Phe Gly Leu Gly His Asn Glu Ala Lys Ala Glu Glu Asn Ser
 40 45 50 55

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60 65 70	
aat gat cag tct agt gat gaa gaa aag aat gat gtg atc aat aat aat	293
Asn Asp Gln Ser Ser Asp Glu Glu Lys Asn Asp Val Ile Asn Asn Asn	
75 80 85	
cag tca ata aac acc gac gat aat aac caa ata att aaa aaa gaa gaa	341
Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile Ile Lys Lys Glu Glu	
90 95 100	
acg aat aac tac gat ggc ata gaa aaa cgc tca gaa gat aga aca gag	389
Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser Glu Asp Arg Thr Glu	
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Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr	
120 125 130 135	
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Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu Val Lys Glu Ser Ser	
140 145 150	
tca gtc gaa tcc tca aat tca tca att gat act gcc caa caa cca tct	533
Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr Ala Gln Gln Pro Ser	
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Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser Lys Ile Lys Glu Ser	
185 190 195	
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Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser Gly Tyr Thr Asn Ile	
220 225 230	
gat gaa aaa att tca aat caa gat gag tta tta aat tta cca ata aat	773
Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn Leu Pro Ile Asn	
235 240 245	

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265 270 275	
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Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His Asp Ala Glu Asn Leu	
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Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys Val Lys Ser Gly Asp	
315 320 325	
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Thr Met Thr Val Asp Ile Asp Lys Asn Thr Val Pro Ser Asp Leu Thr	
330 335 340	
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Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln Ile Thr Tyr Thr Phe	
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Thr Asp Tyr Val Asp Lys Tyr Glu Asn Ile Lys Ala His Leu Lys Leu	
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Lys Ile Thr Phe Glu Thr Pro Glu Gly Tyr Thr Pro Thr Leu Lys His	
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Ser Gly Thr Asn Pro Ala Leu Asp Ser Glu Gly Asn Ser Val Trp Val	
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Ile Thr Asp His Asp Asp Phe Ser Ile Asp Asn Gly Tyr Tyr Asp Asp	
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Gln Ile Ile Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys 100 105 110		
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Ala Thr Phe Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu 130 135 140		
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1080

1085

Lys Asn Lys Asn
1090

B1
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